

SEQUENCE LISTING



<110> Lukyanov, Sergey
Lukyanov, Konstantin
Yanushevich, Yuriy
Savistky, Alexandr
Fradkov, Arcady

<120> Non Aggregating Fluorescent Proteins and
Methods for Using the Same

<130> CLON-067

<150> 10/006,922

<151> 2001-12-04

<150> 60/270,983

<151> 2001-02-21

<160> 31

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 687

<212> DNA

<213> Anemonia majano

<400> 1

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gacatactat ctacagtgtt caagtatgga aatcgatgct ttactgcgta tcctaccagt 240
atgcccgact atttcaaaca agcatttcct gacggaatgt catatgaaag gacttttacc 300
tatgaagatg gaggagtgtc tacagccagt tgggaaataa gccttaaagg caactgcttt 360
gagcaciaat ccacgtttca tggagtgaac tttcctgctg atggacctgt gatggcgaag 420
atgacaactg gttgggaccc atcttttgag aaaatgactg tctgcgatgg aatattgaag 480
ggtgatgtca ccgcgttcct catgctgcaa ggaggtggca attacagatg ccaattccac 540
acttcttaca agacaaaaaa accggtgacg atgccaccaa accatgcggt ggaacatcgc 600
attgcgagga ccgaccttga caaaggtggc aacagtgttc agctgacgga gcacgctgtt 660
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<210> 2

<211> 229

<212> PRT

<213> Anemonia majano

<400> 2

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Gly Asn Gly Lys Pro Tyr Glu Gly Thr Gln Thr Ser Thr Phe Lys Val
          35             40             45
Thr Met Ala Asn Gly Gly Pro Leu Ala Phe Ser Phe Asp Ile Leu Ser
          50             55             60
Thr Val Phe Lys Tyr Gly Asn Arg Cys Phe Thr Ala Tyr Pro Thr Ser
65             70             75             80
    
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Ile	Ser	Leu	Lys	Gly	Asn	Cys	Phe	Glu	His	Lys	Ser	Thr	Phe	His	Gly	
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Val	Asn	Phe	Pro	Ala	Asp	Gly	Pro	Val	Met	Ala	Lys	Met	Thr	Thr	Gly	
	130					135					140					
Trp	Asp	Pro	Ser	Phe	Glu	Lys	Met	Thr	Val	Cys	Asp	Gly	Ile	Leu	Lys	
145					150					155					160	
Gly	Asp	Val	Thr	Ala	Phe	Leu	Met	Leu	Gln	Gly	Gly	Gly	Asn	Tyr	Arg	
				165				170						175		
Cys	Gln	Phe	His	Thr	Ser	Tyr	Lys	Thr	Lys	Lys	Pro	Val	Thr	Met	Pro	
			180					185					190			
Pro	Asn	His	Ala	Val	Glu	His	Arg	Ile	Ala	Arg	Thr	Asp	Leu	Asp	Lys	
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Gly	Gly	Asn	Ser	Val	Gln	Leu	Thr	Glu	His	Ala	Val	Ala	His	Ile	Thr	
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Ser	Val	Val	Pro	Phe												
225																

<210> 3
 <211> 693
 <212> DNA
 <213> Zoanthus sp.

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 aaacaggcta ttaattctgtg tgtggtcgaa ggtggaccat tgccatttgc cgaagacata 180
 ttgtcagctg cctttatgta cggaaacagg gttttcactg aatatcctca agacatagct 240
 gactatttca agaactcgtg tctgtctggt tatacatggg acaggtcttt tctctttgag 300
 gatggagcag tttgcatatg taatgcagat ataacagtga gtgttgaaga aaactgcatg 360
 tatcatgagt ccaaatttta tggagtgaat tttcctgctg atggacctgt gatgaaaaag 420
 atgacagata actgggagcc atcctgcgag aagatcatac cagtacctaa gcaggggata 480
 ttgaaagggg atgtctccat gtacctcctt ctgaaggatg gtgggcgttt acggtgccaa 540
 ttcgacacag tttaaaagc aaagtctgtg ccaagaaaga tgccggactg gcacttcatac 600
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<210> 4
 <211> 231
 <212> PRT
 <213> Zoanthus sp.

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 Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Ala Ile Asn Leu Cys Val
 35 40 45
 Val Glu Gly Gly Pro Leu Pro Phe Ala Glu Asp Ile Leu Ser Ala Ala
 50 55 60
 Phe Asn Tyr Gly Asn Arg Val Phe Thr Glu Tyr Pro Gln Asp Ile Ala
 65 70 75 80
 Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Asp Arg Ser
 85 90 95
 Phe Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Ala Asp Ile Thr

			100					105					110				
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Val	Asn	Phe	Pro	Ala	Asp	Gly	Pro	Val	Met	Lys	Lys	Met	Thr	Asp	Asn		
	130					135					140						
Trp	Glu	Pro	Ser	Cys	Glu	Lys	Ile	Ile	Pro	Val	Pro	Lys	Gln	Gly	Ile		
145					150					155					160		
Leu	Lys	Gly	Asp	Val	Ser	Met	Tyr	Leu	Leu	Leu	Lys	Asp	Gly	Gly	Arg		
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Leu	Arg	Cys	Gln	Phe	Asp	Thr	Val	Tyr	Lys	Ala	Lys	Ser	Val	Pro	Arg		
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Lys	Met	Pro	Asp	Trp	His	Phe	Ile	Gln	His	Lys	Leu	Thr	Arg	Glu	Asp		
	195						200				205						
Arg	Ser	Asp	Ala	Lys	Asn	Gln	Lys	Trp	His	Leu	Thr	Glu	His	Ala	Ile		
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Ala	Ser	Gly	Ser	Ala	Leu	Pro											
225					230												

<210> 5
 <211> 865
 <212> DNA
 <213> Zoanthus sp.

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gtgctgcaac ggacataaat ttgtgatcac gggcgaaggc attggatata cgttcaaagg 180
gaaacagact attaactctgt gtgtgatcga agggggacca ttgccatttt ccgaagacat 240
attgtcagct ggctttaagt acggagacag gatttttact gaatatcctc aagacatagt 300
agactatttc aagaactcgt gtcctgctgg atatacatgg ggcaggtctt ttctctttga 360
ggatggagca gtctgcatat gcaatgtaga tataacagtg agtgtcaaag aaaactgcat 420
ttatcataag agcatattta atggaatgaa ttttctgtct gatggacctg tgatgaaaaa 480
gatgacaact aactgggaag catcctgcga gaagatcatg ccagtaccta agcaggggat 540
actgaaaggg gatgtctcca tgtacctcct tctgaaggat ggtgggctgt accggtgcca 600
gttcgacaca gtttaciaaag caaagtctgt gccaaagtaag atgccggagt ggcacttcat 660
ccagcataag ctctccctgt aagaccgcag cgatgctaag aatcagaagt ggcagctgac 720
agagcatgct attgcattcc cttctgcctt ggcctgataa gaatgtagtt ccaacatttt 780
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<210> 6
 <211> 230
 <212> PRT
 <213> Zoanthus sp.

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		20					25						30				
Gly	Ile	Gly	Tyr	Pro	Phe	Lys	Gly	Lys	Gln	Thr	Ile	Asn	Leu	Cys	Val		
	35					40					45						
Ile	Glu	Gly	Gly	Pro	Leu	Pro	Phe	Ser	Glu	Asp	Ile	Leu	Ser	Ala	Gly		
	50				55					60							
Phe	Lys	Tyr	Gly	Asp	Arg	Ile	Phe	Thr	Glu	Tyr	Pro	Gln	Asp	Ile	Val		
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Asp	Tyr	Phe	Lys	Asn	Ser	Cys	Pro	Ala	Gly	Tyr	Thr	Trp	Gly	Ser	Phe		
			85			90							95				
Leu	Phe	Glu	Asp	Gly	Ala	Val	Cys	Ile	Cys	Asn	Val	Asp	Ile	Thr	Val		

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Ser	Val	Lys	Glu	Asn	Cys	Ile	Tyr	His	Lys	Ser	Ile	Phe	Asn	Gly	Met		
		115					120					125					
Asn	Phe	Pro	Ala	Asp	Gly	Pro	Val	Met	Lys	Lys	Met	Thr	Thr	Asn	Trp		
	130					135					140						
Glu	Ala	Ser	Cys	Glu	Lys	Ile	Met	Pro	Val	Pro	Lys	Gln	Gly	Ile	Leu		
145				150						155					160		
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		165					170							175			
Arg	Cys	Gln	Phe	Asp	Thr	Val	Tyr	Lys	Ala	Lys	Ser	Val	Pro	Ser	Lys		
		180					185						190				
Met	Pro	Glu	Trp	His	Phe	Ile	Gln	His	Lys	Leu	Leu	Arg	Glu	Asp	Arg		
	195						200					205					
Ser	Asp	Ala	Lys	Asn	Gln	Lys	Trp	Gln	Leu	Thr	Glu	His	Ala	Ile	Ala		
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Phe	Pro	Ser	Ala	Leu	Ala												
225					230												

<210> 7
 <211> 678
 <212> DNA
 <213> Discosoma sp

<400> 7
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 cacaacaccg tgaagctgaa ggtgaccaag ggcggccccc tgcccttcgc ctgggacatc 180
 ctgtcccccc agttccagta cggctccaag gtgtacgtga agcaccocgc cgacatcccc 240
 gactacaaga agctgtcctt ccccgagggc ttcaagtggg agcgcgtgat gaacttcgag 300
 gacggcggcg tggtagaccg gacccaggac tcctccctgc aggacggctg cttcatctac 360
 aaggtgaagt tcatcggcgt gaacttcccc tccgacggcc ccgtgatgca gaagaagacc 420
 atgggctggg aggccctccac cgagcgccctg taccoccgcg acggcgtgct gaaggcgag 480
 atccacaagg ccctgaagct gaaggacggc ggccactacc tggtaggagtt caagtccatc 540
 tacatggcca agaagcccgt gcagctgccc ggctactact acgtggactc caagtgggac 600
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 caccacctgt tcctgtaa 678

<210> 8
 <211> 225
 <212> PRT
 <213> Discosoma sp.

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 Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val
 35 40 45
 Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln
 50 55 60
 Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro
 65 70 75 80
 Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
 85 90 95
 Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser
 100 105 110
 Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn
 115 120 125

Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu
 130 135 140
 Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu
 145 150 155 160
 Ile His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu
 165 170 175
 Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr
 180 185 190
 Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr
 195 200 205
 Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe
 210 215 220
 Leu
 225

<210> 9
 <211> 696
 <212> DNA
 <213> Anemonia sulcata

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 atgaagatag aggtcatcga aggaggtcca ttgccatttg ccttccacat tttgtcaacg 180
 agttgtatgt acggtagtaa ggccttcacg aagtatgtgt caggaattcc tgactacttc 240
 aagcagtcct tccctgaagg ttttacttgg gaaagaacca caacctacga ggatggaggc 300
 tttcttacag ctcatcagga cacaagccta gatggagatt gcctcgttta caaggtcaag 360
 attcttggtg ataattttcc tgctgatggc cccgtgatgc agaacaaagc aggaagatgg 420
 gagccatcca ccgagatagt ttatgaagtt gacgggtgtcc tgcgtggaca gtctttgatg 480
 gcccttaagt gccctggtgg tcgtcatctg acttgccatc tccatactac ttacaggtcc 540
 aaaaaaccag ctgctgcctt gaagatgccg ggatttcatt ttgaagatca tcgcatcgag 600
 ataatggagg aagttgagaa aggcaagtgc tataaacagt acgaagcagc agtgggcagg 660
 tactgtgatg ctgctccatc caagcttggg cataac 696

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 <211> 232
 <212> PRT
 <213> Anemonia sulcata

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 Asn Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly
 35 40 45
 Gly Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr
 50 55 60
 Gly Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe
 65 70 75 80
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
 85 90 95
 Glu Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly
 100 105 110
 Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Gln Asn Lys Ala Gly Arg Trp Glu Pro Ala Thr
 130 135 140
 Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met

145		150		155		160									
Ala	Leu	Lys	Cys	Pro	Gly	Gly	Arg	His	Leu	Thr	Cys	His	Leu	His	Thr
		165		170		175									
Thr	Tyr	Arg	Ser	Lys	Lys	Pro	Ala	Ala	Ala	Leu	Lys	Met	Pro	Gly	Phe
		180		185		190									
His	Phe	Glu	Asp	His	Arg	Ile	Glu	Ile	Met	Glu	Glu	Val	Glu	Lys	Gly
		195		200		205									
Lys	Cys	Tyr	Lys	Gln	Tyr	Glu	Ala	Ala	Val	Gly	Arg	Tyr	Cys	Asp	Ala
		210		215		220									
Ala	Pro	Ser	Lys	Leu	Gly	His	Asn								
225				230											

<210> 11
 <211> 678
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hybrid coding sequence

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 cactgcagcg tgaagctcat ggtgaccaag ggcgcccccc tccccttcgc cttcgacatc 180
 ctcagccccc agttccagta cggcagcaag gtgtacgtga agcaccgccg cgacatcccc 240
 gactacaaga agctcagctt ccccagaggc ttcaagtggg agcgggtgat gaacttcgag 300
 gacggcggcg tggtgaccgt gagccaggac agcagcctca aggacggctg cttcatctac 360
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 cggggctggg aggccagcag cgagcggctc taccgccggg acggcgtgct caagggcgac 480
 atccacatgg cctccggct cgagggcggc ggccactacc tcgtggagtt caagagcatc 540
 tacatggcca agaagcccgt gcagctcccc ggctactact acgtggacag caagctcgac 600
 atcaccagcc acaacgagga ctacaccatc gtggagcagt acgagcggac cgagggccgg 660
 caccacctct tcctctga 678

<210> 12
 <211> 225
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hybrid protein

<400> 12
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 35 40 45
 Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser Pro Gln
 50 55 60
 Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro
 65 70 75 80
 Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
 85 90 95
 Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Ser Gln Asp Ser Ser
 100 105 110
 Leu Lys Asp Gly Cys Phe Ile Tyr Glu Val Lys Phe Ile Gly Val Asn
 115 120 125

Phe	Pro	Ser	Asp	Gly	Pro	Val	Met	Gln	Arg	Arg	Thr	Arg	Gly	Trp	Glu
130						135					140				
Ala	Ser	Ser	Glu	Arg	Leu	Tyr	Pro	Arg	Asp	Gly	Val	Leu	Lys	Gly	Asp
145					150					155					160
Ile	His	Met	Ala	Leu	Arg	Leu	Glu	Gly	Gly	Gly	His	Tyr	Leu	Val	Glu
				165						170					175
Phe	Lys	Ser	Ile	Tyr	Met	Ala	Lys	Lys	Pro	Val	Gln	Leu	Pro	Gly	Tyr
			180					185					190		
Tyr	Tyr	Val	Asp	Ser	Lys	Leu	Asp	Ile	Thr	Ser	His	Asn	Glu	Asp	Tyr
		195					200					205			
Thr	Ile	Val	Glu	Gln	Tyr	Glu	Arg	Thr	Glu	Gly	Arg	His	His	Leu	Phe
	210					215					220				
Leu															
225															

<210> 13
 <211> 675
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> non-aggregating mutant

<400> 13

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<210> 14
 <211> 678
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> non-aggregating mutant

<400> 14

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cacaacaccg	tgaagttgaa	ggtgaccaag	ggcgcccccc	tgcccttcgc	ctgggacatc	180
ctgtcccccc	agttccagta	cggctccaag	gtgtacgtga	agcaccgccg	cgacatcccc	240
gactacaaga	agctgtcctt	ccccgagggc	ttcaagtggg	agcgcgatgat	gaacttcgag	300
gacggcgggc	tggcgaccgt	gacccaggac	tcctccctgc	aggacggctg	cttcatctac	360
aaggtgaagt	tcacgcggcg	gaacttcccc	tccgacggcc	ccgtgatgca	gaagaagacc	420
atgggctggg	aggcctccac	cgagcgccctg	tacccccgcg	acggcggtgct	gaagggcgag	480
atccacaagg	ccctgaagct	gaaggacggc	ggccactacc	tgggtggagtt	caagtccatc	540
tacatggcca	agaagcccgt	gcagctgccc	ggctactact	acgtggacac	caagctggac	600
atcacctccc	acaacgagga	ctacaccatc	gtggagcagt	acgagcgcac	cgagggccgc	660
caccacctgt	tcctgtaa					678

<210> 15
 <211> 705
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> non-aggregating mutant

<400> 15
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 gggaaacagg ctattaatct gtgtgtgggtc gaagggtggac cattgccatt tgcogaagac 180
 atattgtcag ctgcctttat gtacggaaac agggttttca ctgaatatcc tcaagacata 240
 gttgactatt tcaagaactc gtgtcctgct ggatatacat gggacaggtc ttttctcttt 300
 gaggatggag cagtttgcac atgtaatgca gatataacag tgagtgttga agaaaactgc 360
 atgtatcatg agtccaaatt ctatggagtg aattttcctg ctgatggacc tgtgatgaaa 420
 aagatgacag ataactggga gccatcctgc gagaagatca taccagtacc taagcagggg 480
 atattgaaag gggatgtctc catgtacctc cttctgaagg atgggtgggcg tttacgggtgc 540
 caattcgaca cagttttacaa agcaaagtct gtgccaagaa agatgccgga ctggcacttc 600
 atccagcata agctcaccgc tgaagaccgc agcgatgcta agaatacagaa atggcatctg 660
 acagaacatg ctattgcata cggatctgca ttgccctgaa agctt 705

<210> 16
 <211> 230
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> non-aggregating mutant

<400> 16
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 Met Glu Gly Cys Val Asn Gly His Lys Phe Val Ile Thr Gly Glu Gly
 20 25 30
 Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn Leu Cys Val Ile
 35 40 45
 Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala Gly Phe
 50 55 60
 Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr Pro Gln Asp Ile Val Asp
 65 70 75 80
 Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gly Arg Ser Phe
 85 90 95
 Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Val Asp Ile Thr Val
 100 105 110
 Ser Val Lys Glu Asn Cys Ile Tyr His Lys Ser Ile Phe Asn Gly Val
 115 120 125
 Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr Asn Trp
 130 135 140
 Glu Ala Ser Cys Glu Lys Ile Met Pro Val Pro Lys Gln Gly Ile Leu
 145 150 155 160
 Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Tyr
 165 170 175
 Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Ser Lys
 180 185 190
 Met Pro Glu Trp His Phe Ile Gln His Lys Leu Leu Arg Glu Asp Arg
 195 200 205
 Ser Asp Ala Lys Asn Gln Lys Trp Gln Leu Thr Glu His Ala Ile Ala
 210 215 220
 Phe Pro Ser Ala Leu Ala

<210> 17
 <211> 705
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> non-aggregating mutant

<400> 17
 ggatccgccc acagcgagca cggcctgacc gaggagatga ccatgaagta ccacatggag 60
 ggctgcgtga acggccacaa gttcgtgata accggcgagg gcatcggtta ccccttcaag 120
 ggcaagcaga ccatcaacct gtgcgtgata gagggcggcc ccctgccctt cagcgaggac 180
 atcctgagcg ccggcttcaa gtacggcgac cggatcttca ccgagtaccc ccaggacatc 240
 gtggactact tcaagaacag ctgccccgcc ggctacacct ggggccggag cttcctgttc 300
 gaggacggcg ccgtgtgcat ctgtaacgtg gacatcaccc tgagcgtgaa ggagaactgc 360
 atctaccaca agagcatctt caacggcgtg aacttccccg ccgacggccc cgtgatgaag 420
 aagatgacca ccaactggga ggccagctgc gagaagatca tgcccgtgcc taagcagggc 480
 atcctgaagg gcgacgtgag catgtacctg ctgctgaagg acggcggccg gtaccggtgc 540
 cagttcgaca ccgtgtacaa ggccaagagc gtgcccagca agatgcccga gtggcacttc 600
 atccagcaca agctgctgcg ggaggaccgg agcgacgcca agaaccagaa gtggcagctg 660
 accgagcacg ccatcgccctt ccccgcgccc ctggcctgaa agctt 705

<210> 18
 <211> 230
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> non-aggregating mutant

<400> 18
 Ala His Ser Glu His Gly Leu Thr Glu Glu Met Thr Met Lys Tyr His
 1 5 10 15
 Met Glu Gly Cys Val Asn Gly His Lys Phe Val Ile Thr Gly Glu Gly
 20 25 30
 Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn Leu Cys Val Ile
 35 40 45
 Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala Gly Phe
 50 55 60
 Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr Pro Gln Asp Ile Val Asp
 65 70 75 80
 Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gly Arg Ser Phe
 85 90 95
 Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Val Asp Ile Thr Val
 100 105 110
 Ser Val Lys Glu Asn Cys Ile Tyr His Lys Ser Ile Phe Asn Gly Val
 115 120 125
 Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr Asn Trp
 130 135 140
 Glu Ala Ser Cys Glu Lys Ile Met Pro Val Pro Lys Gln Gly Ile Leu
 145 150 155 160
 Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Tyr
 165 170 175
 Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Ser Lys
 180 185 190
 Met Pro Glu Trp His Phe Ile Gln His Lys Leu Leu Arg Glu Asp Arg
 195 200 205

Ser Asp Ala Lys Asn Gln Lys Trp Gln Leu Thr Glu His Ala Ile Ala
 210 215 220
 Phe Pro Ser Ala Leu Ala
 225 230

<210> 19
 <211> 690
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> non-aggregating mutant

<400> 19
 atggccctgt ccaacgagtt catcgggcgac gacatgaaga tgacctacca catggacggc 60
 tgcgtgaacg gccactactt caccgtgaag ggcgagggca gcggcaagcc ctacgagggc 120
 acccagacct ccaccttcaa ggtgaccatg gccaacggcg gccccctggc cttctccttc 180
 gacatcctgt ccacgtgtt catgtacggc aaccgtgtct tcaccgccta cccaccagc 240
 atgcccgaact acttcaagca ggccttcccc gacggcatgt cctacgagag aaccttcacc 300
 tacgaggacg gcggcggtggc caccgccagc tgggagatca gcctgaaggg caactgcttc 360
 gagcacaagt ccaccttcca cggcggtgaac ttccccgccg acggccccgt gatggccaag 420
 aagaccaccg gctgggaccc ctccctcgag aagatgaccg tgtgcgacgg catcttgaag 480
 ggcgacgtga cgccttcct gatgctgcag ggcgggcgga actacagatg ccagttccac 540
 acctctaca agaccaagaa gcccgtgacc atgcccccca accacgtggt ggagcaccgc 600
 atcgccagaa ccgacctgga caagggcggc aacagcgtgc agctgaccga gcacgccgtg 660
 gccacatca cctccgtggt gcccttctga 690

<210> 20
 <211> 229
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> non-aggregating mutant

<400> 20
 Met Ala Leu Ser Asn Glu Phe Ile Gly Asp Asp Met Lys Met Thr Tyr
 1 5 10 15
 His Met Asp Gly Cys Val Asn Gly His Tyr Phe Thr Val Lys Gly Glu
 20 25 30
 Gly Ser Gly Lys Pro Tyr Glu Gly Thr Gln Thr Ser Thr Phe Lys Val
 35 40 45
 Thr Met Ala Asn Gly Gly Pro Leu Ala Phe Ser Phe Asp Ile Leu Ser
 50 55 60
 Thr Val Phe Met Tyr Gly Asn Arg Cys Phe Thr Ala Tyr Pro Thr Ser
 65 70 75 80
 Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr Glu
 85 90 95
 Arg Thr Phe Thr Tyr Glu Asp Gly Gly Val Ala Thr Ala Ser Trp Glu
 100 105 110
 Ile Ser Leu Lys Gly Asn Cys Phe Glu His Lys Ser Thr Phe His Gly
 115 120 125
 Val Asn Phe Pro Ala Asp Gly Pro Val Met Ala Lys Lys Thr Thr Gly
 130 135 140
 Trp Asp Pro Ser Phe Glu Lys Met Thr Val Cys Asp Gly Ile Leu Lys
 145 150 155 160
 Gly Asp Val Thr Ala Phe Leu Met Leu Gln Gly Gly Gly Asn Tyr Arg
 165 170 175
 Cys Gln Phe His Thr Ser Tyr Lys Thr Lys Lys Pro Val Thr Met Pro

Leu	Glu	Cys	Pro	Gly	Gly	Arg	His	Leu	Thr	Cys	His	Leu	His	Thr	Thr
				165					170					175	
Tyr	Arg	Ser	Lys	Lys	Pro	Ala	Ser	Ala	Leu	Lys	Met	Pro	Gly	Phe	His
			180					185					190		
Phe	Glu	Asp	His	Arg	Ile	Glu	Ile	Leu	Glu	Glu	Val	Glu	Lys	Gly	Lys
		195				200						205			
Cys	Tyr	Lys	Gln	Tyr	Glu	Ala	Ala	Val	Gly	Arg	Tyr	Cys	Asp	Ala	Ala
	210					215					220				
Pro	Ser	Lys	Leu	Gly	His	Asn									
225					230										

<210> 23

<211> 654

<212> DNA

<213> Artificial Sequence

<220>

<223> non-aggregating mutant

<400> 23

gagggcaccg	tgaacggcca	ctacttcaag	tgcaccggca	agggcgaggg	caacccccctc	60
gagggcaccc	aggagatgaa	gatcgagggtg	atcgagggcg	gccccctgcc	cttcgccttc	120
cacatcctgt	ccacctcctg	catgtacggc	tccaaggcct	tcatcaagta	cgtgtccggc	180
atccccgact	acttcaagca	gtccctcccc	gagggcttca	cctgggagcg	caccaccacc	240
tacgaggacg	gcggttcct	gaccgcccac	caggacacct	ccctggacgg	cgactgctg	300
gtgtacaagg	tgaagatcct	gggcaacaac	ttccccgccg	acggccccgt	gatgcagaac	360
aaggccggcc	gctgggagcc	ctccaccgag	atcgtgtacg	aggtggacgg	cgtgctgcgc	420
ggccagtcca	gcatggccct	ggagtgcccc	ggcggtcgcc	acctgacctg	ccacctgcac	480
accacctacc	gctccaagaa	gcccgcctcc	gccctgaaga	tgcccggctt	ccacttcgag	540
gaccaccgca	tcgagatcct	ggaggaggtg	gagaagggca	agtgctacaa	gcagtacgag	600
gccgccgtgg	gccgctactg	cgacgccgcc	ccctccaagc	tgggccacaa	ctga	654

<210> 24

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> non-aggregating mutant

<400> 24

Met	Ala	Ser	Leu	Leu	Thr	Glu	Thr	Met	Pro	Phe	Arg	Thr	Thr	Ile	Glu
1			5					10						15	
Gly	Thr	Val	Asn	Gly	His	Tyr	Phe	Lys	Cys	Thr	Gly	Lys	Gly	Glu	Gly
			20					25					30		
Asn	Pro	Leu	Glu	Gly	Thr	Gln	Glu	Met	Lys	Ile	Glu	Val	Ile	Glu	Gly
		35				40					45				
Gly	Pro	Leu	Pro	Phe	Ala	Phe	His	Ile	Leu	Ser	Thr	Ser	Cys	Met	Tyr
	50				55						60				
Gly	Ser	Lys	Ala	Phe	Ile	Lys	Tyr	Val	Ser	Gly	Ile	Pro	Asp	Tyr	Phe
65					70					75				80	
Lys	Gln	Ser	Leu	Pro	Glu	Gly	Phe	Thr	Trp	Glu	Arg	Thr	Thr	Thr	Tyr
			85					90						95	
Glu	Asp	Gly	Gly	Phe	Leu	Thr	Ala	His	Gln	Asp	Thr	Ser	Leu	Asp	Gly
		100					105					110			
Asp	Cys	Leu	Val	Tyr	Lys	Val	Lys	Ile	Leu	Gly	Asn	Asn	Phe	Pro	Ala
	115						120					125			
Asp	Gly	Pro	Val	Met	Gln	Asn	Lys	Ala	Gly	Arg	Trp	Glu	Pro	Ser	Thr
	130					135					140				

Glu	Ile	Val	Tyr	Glu	Val	Asp	Gly	Val	Leu	Arg	Gly	Gln	Ser	Ser	Met
145					150					155					160
Ala	Leu	Glu	Cys	Pro	Gly	Gly	Arg	His	Leu	Thr	Cys	His	Leu	His	Thr
				165						170					175
Thr	Tyr	Arg	Ser	Lys	Lys	Pro	Ala	Ser	Ala	Leu	Lys	Met	Pro	Gly	Phe
			180					185					190		
His	Phe	Glu	Asp	His	Arg	Ile	Glu	Ile	Leu	Glu	Glu	Val	Glu	Lys	Gly
		195					200					205			
Lys	Cys	Tyr	Lys	Gln	Tyr	Glu	Ala	Ala	Val	Gly	Arg	Tyr	Cys	Asp	Ala
	210					215					220				
Ala	Pro	Ser	Lys	Leu	Gly	His	Asn								
225					230										

<210> 25
 <211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> non-aggregating mutant fragment

Met	Arg	Ser	Ser	Lys	Asn	Val	Ile	Lys	Glu	Phe	Met	Arg	Phe	Lys	Val
1				5					10					15	
Arg	Met	Glu	Gly	Thr	Val	Asn	Gly	His	Glu						
			20					25							

<210> 26
 <211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> non-aggregating mutant fragment

Met	Ser	Cys	Ser	Lys	Asn	Val	Ile	Lys	Glu	Phe	Met	Arg	Phe	Gln	Val
1				5					10					15	
Arg	Met	Glu	Gly	Thr	Val	Asn	Gly	His	Glu						
			20					25							

<210> 27
 <211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> non-aggregating mutant fragment

Met	Ala	Gln	Ser	Lys	His	Gly	Leu	Thr	Lys	Glu	Met	Thr	Met	Lys	Tyr
1				5					10					15	
Arg	Met	Glu	Gly	Cys	Val	Asp	Gly	His	Lys						
			20					25							

<210> 28

<211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> non-aggregating mutant fragment

<400> 28
 Met Ala His Ser Lys His Gly Leu Lys Glu Glu Met Thr Met Lys Tyr
 1 5 10 15
 His Met Glu Gly Cys Val Asn Gly His Lys
 20 25

<210> 29
 <211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> non-aggregating mutant fragment

<400> 29
 Met Ala Leu Ser Asn Lys Phe Ile Gly Asp Asp Met Lys Met Thr Tyr
 1 5 10 15
 His Met Asp Gly Cys Val Asn Gly His Tyr
 20 25

<210> 30
 <211> 23
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> non-aggregating mutant fragment

<400> 30
 Met Ala Ser Phe Leu Lys Lys Thr Met Pro Phe Lys Thr Thr Ile Glu
 1 5 10 15
 Gly Thr Val Asn Gly His Tyr
 20

<210> 31
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> purification tag

<400> 31
 Met Arg His His His His His His Gly Ser
 1 5 10